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Result
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Maximum Match 100%
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Perfect score:
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Copyright
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(without alignments)
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ALIGNMENTS

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C;Accession: H72652
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 6, 83-101, 1999
DNA Res. 6, 83-101, 1999
DNA Res. 6, 80-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Title: Complete genome: A72450; MUID:99310339; PMID:10382966
A;Accession: H72652
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H72652
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                                               A; Gene: APE0653
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein APE0653 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable potassium-efflux system protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
                                                                                                                            A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79624.1; A;Experimental source: strain K1
                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AL590842; PIDN:CAC89052.1; PID:g15978292; GSPDB:GN00175
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A; Residues: 1-602 < KUR>
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Best Local
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20 AVPIAQR 26
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                                                  Aeropyrum pernix hypothetical protein APE0653
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Pred. No.
  Score 29;
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DB 2;
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Length 211;
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RESULT 4
$77102
$77102
Synchetical protein slr1865 - Synechocystis - F
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: $77102
P:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;
P:Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamaɗ
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A;Start
                           RESULT
C75085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable arginine deiminase - Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_C;Accession: D70602
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                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-420 <KAN>
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A; Status: nucleic
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A; Residues: 1-402 <C
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                                                                                                                                                                                                                                                                                                                                               A; Reference number: S74322; MUID: 97061201;
                                                                                                                                                                                                                                                                                                                                                                           A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
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2; Mis
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Yamada, M.; Yasud
                                                                                                                                                                                                                                                  June
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                                                                              RESULT
G84120
                                                                                                                                                                                ribose 5-phosphate epimerase (pentose phosphate) BH3767 [imported] - Bacillus C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                       A; Molecule type: DNA
A; Residues: 1-145 <STO>
                                                                                                                                                                   C; Accession: G84120
                          A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07486.1; GSPDB:G
                                                                      A; Status: preliminary
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R.; Masui, N.; Fuji,

F . ;

halodur

Bacillus halodurans

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DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the F
A;Title: Complete Genomic Sequence of the F
                                                                                                                               A; Gene: alr0205
C; Superfamily: recQ protein; recQ
                                                                                                                                                                                                                                                                                                                                                           ATP-dependent DNA helicase [imported] - Nostoc sp. C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 C;Rocession: AE1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
AE1832
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R; anonymous, Genoscope
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C; Date: 20-Aug-1999 #sequence_revision
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                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-718 <KUR>
                                                                                                                                                                                                                                                                                                                               R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa,
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C; Superfamily:
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A; Residues: 1-437 <KAW>
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                                                                                                                                                                                 A;Cross-references: GB:BA000019; PIDN:BAB77729.1; A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                A;Reference number: AB1807;
A;Accession: AE1832
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                                                                                                                                                                               A; Experimental source: strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PAB1660 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                Nakazaki, N.; Shimpo, S.
NA Res. 8, 205–213, 2001
                                                                                                                                                               ; Genetics:
                                                                                Query Match
Best Local
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Best Local
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SVPVAQK
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71.48;
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                                                                                                Score 29;
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PMID:11759840
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, M.; Yasuda,
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AVPIIQK 114

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A; Gene: PH1921
C; Superfamily:
C; Keywords: ami
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DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71206
A;Accession: G71206
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C; Genetics:
A; Gene: BH3767
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                             hypothetical protein alr2582 [imported] - Nostoc sp. (strain PCC 7120) c;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 c;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 c;Accession: AG2128
                                                                                                                                                                                                                                         R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentou A; Reference number: AB1807; MUID:21595285; PMID:1175A; Accession: AG2128
                                                                                                                                       A; Experimental source: strain C; Genetics:
                õ
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A; Residues: 1-323 <KUR>
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Kawarabayasi, Y.; Sawada, M.; M.; Ohfuku, Y.; Funahashi, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 03-Jun-2002
C;Accession: G71206
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C; Species: Pyrococcus horikoshii
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aminoacyl-tRNA synthetase; ligase;
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57.1%;
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85.7%;
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71.4%;
                                                                                                                                                                                                                                                        Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
7; MUID:21595285; PMID:11759840
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Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
                                                Score 28; DB
Pred. No. 69;
0; Mismatches
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Pred. No. 64;
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M.; Yamada, M.; Yasuda, I
                                                                                 Length 323;
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hypothetical protein alr3027 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD2184
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquentazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabatz Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabatz DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
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Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A;Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus
A;Reference number: A94027; MUID:85166175; PMID:2984661
A;Accession: A03671
A;Accession: A03671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EZ protein - cottontail rabbit papillomavirus C;Species: cottontail rabbit papillomavirus C;Date: 28-Aug-1985 #sequence_revision 28-Aug-C;Accession: A03671
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: papillomavirus
C;Keywords: early protein
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C;Superfamily: mammalian tryptophan-tRNA ligase;
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A; Accession: C75020
A; Status: preliminary
                    A; Reference number: AB1807; A; Accession: AD2184
                                                                                                                                                                                                                                                                AD2184
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A; Residues: 1-390 <GIR>
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5; Conser
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85.7%;
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Pred.
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Pred. No. 85;
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A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-656 <HEI>
                                                                                                                                                                                                                                                                                                     A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: B82056
                                                                                                                                                                                                                                                                                                                                                                  R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            glutathione-regulated potassium-efflux system protein KefB VC2606 [imported] C;Speckes: Vibrio cholerae C;Deckes: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaew, White, O.; Salsbarg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S. A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:BA000019; PIDN:BAB74726.1; PID:g17132121; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                 A;Map position: 1 {\sf C};Superfamily: glutathione-regulated potassium efflux system protein kefC
                                                                                                                                                                                 A;Cross-references: GB:AE004327; GB:AE003852; NID:g9657185; PIDN:AAF95747.1; GSPDB:GN00 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pyruvate kinase [imported] - Caulobacter crescentus
c;Species: Caulobacter crescentus
c;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: D87503
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A; Residues: 1-476 <STO>
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71.4%;
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83.3%;
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1; Mismatche
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DB 2; L.
1.5e+02;
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Search completed: September 12, Job time: 43 secs
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C; Superfamily: S
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                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-845 <MOO>
A;Cross references: EMBL;AL035592; PIDN:CAB38163.1; GSPDB:GN00068; SPDB:SPCC1393.07c
A;Experimental source: strain 972h-; cosmid c1393
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, submitted to the EMBL Data Library, February 1999 A;Reference number: 221940 A;Accession: T40955
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Perfect score:
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19.014 Million cell updates/sec
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       1 Q8R1DB
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Q96FU5
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Q9vfg4 drosophila
Q8tbm0 homo sapien
Q9h8k8 homo sapien
Q9f6u5 homo sapien
Q8fjc4 yersinia pe
Q8jz11 beet wester
Q9nfp7 ceratitis r
                Q9yec2 aeropyrum p
Q977m5 uncultured
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Q9Y066	Q9A6N6	Q8YSQ7	Q979W5	Q98DE7	Q9ICK8	Q9IES1	Q8BR14	Q8ETN2	Q8YTY1	Q8CIF0	Q9NH08	Q8DWG7	Q85062	Q9K6G2	Q95ZI1	075592	Q8AW10	Q8PEP6	Q8LK00	Q8Z093	Q9UZS2	Q56470	Q8E2F6	Q8E7W4	Q9EU98	Q9ETV8	Q9F9X2	P73615
Q9y066 trypanosoma	Q9a6n6 caulobacter	Q8ysq7 anabaena sp	Q979w5 thermoplasm		Q9ick8 cottontail .	cot		oceanoba	Q8ytyl anabaena sp	Q8cif0 mus musculu	Q		Q85062 cottontail	Q9k6g2 bacillus ha		075592 homo sapien	Q8aw10 brachydanio				Q9uzs2 pyrococcus	Q56470 uncultured		Q8e7w4 streptococc			ß	P73615 synechocyst

ALIGNMENTS

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RESULT 1
Q8R1D8
ID Q8R1
AC Q8R1
DT 01-J
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DT 01-J
DT 01-J
C Simi
OS Mus
OC Euka
OC Mamm
OX NCBII
RN [1]
RN [1]
RP SEQU
RC TISSS
RA Stra
RL Subm
DR EMBI
RESULT 2
Q8BW93
ID Q8BW
AC Q8BW
DT 01-M
DT 01-
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Best Local Similarity
Matches 7; Conserv
                                                          Q8BW93 PRELIMINARY; PRT; 344 AA.
Q8BW93;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q2-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8R1D8 PRELIMINARY; PRT; 157 AA. Q8R1D8; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) similar to RIKEN CDNA 0610041G12 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC034780; AAH24780.1; -
SEQUENCE 157 AA; 17799 MW; 0F67319F05EAC6E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 AVPIAOK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 9.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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SOR RT

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RESULT QUVEGE OCCUPANT OCCUPAN
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C 09VFG4;

C 09VFG4;

DT 01-MAX-2000 (TrEMBLrel. 13, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OFGA;

C 09VFG4;

DT 01-OCT-2002 (TrEMBLrel. 23, Last annotation update)

DE CG7362 protein.

GN CG7362.

OS Drosophila melanogaster (Fruit fly).

OC Ewaryota; Metazoa; Arthropoda; Hexapoda; Insecta

OC Neoptera; Endopterygota; Diptera; Brachycera; Mus
RX MEDLINE-2019606; pubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Bassam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Bokstein P., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Riamos I., Simpson M., Skupski M.P., Smith T.,
Ra Palackin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of the mouse transcriptome based 60,770 full-length CDNAs.";
Nature 420:563-573(2002)
EMBL; AK053187; BAC35303.1; -.
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7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Last sequence update)
Last annotation updat
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Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508FFD23F01B31C8
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era; Muscomorpha;
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; "Annotation of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan | Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Goralez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., Williams T.C., Moy M., Murphy B., Helson C., Nelson K.A., Nunoo Pacleb J., Paragas V., Park S., Patel S., Ffeiffer B., Phouanenavong S., Pittnan G.S., Puri V., Richards S., Scheeler Phouanenavong S., Pittnan G.S., Puri V., Richards S., Scheeler Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                   Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                   Q8TBMO;
Q1-JUN-2002 (TrEMBLrel.
Q1-JUN-2002 (TrEMBLrel.
Q1-MAR-2003 (TrEMBLrel.
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TIGRFAMS; TIGR01064; pyruv_kin; 1.
PROSITE; PS00110; PYRUVATE_KINASE; 1.
SEQUENCE 1010 AA; 113769 MW; 9D04.
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HSSP; P14178; 1EOT.
FlyBaco. pression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Gibbs R.A., Myers
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nce 287:2185-2195(2000).
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Celniker
2000)
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6; Conser
                                                                                                                                                                                                                                                                                                           AVPLAQK
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                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
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Primates;
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                                                                                          Last sequence update)
Last annotation updat
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1; Mismatches
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Catarrhini;
                        Craniata; Vertebrata;
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Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter C.J.;
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A Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
A Tanase T., Nomura Y., Togiya S., Kawai F., Hara R., Takeuchi K.,
A Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
A Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AK023550; BAB14608.1; -.
BR EMBL; AK023550; BAB14608.1; -.
BR InterPro; IPR001278; Arg_trNA-synt_IC.
InterPro; IPR001278; Arg_trNA-synt_IC.
BR InterPro; IPR001278; Arg_trNA-synt_IC.
BR InterPro; IPR001278; Arg_trNA-synt_IC.
BR FAINTS; PR01038; TRNASYNTHARG.
BR FRINTS; PR01038; TRNASYNTHARG.
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Matches (
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                            Q96FU5;
01-DEC-2001
01-DEC-2001
01-MAR-2003
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ13488.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chrimates; Catarrhini; Hominidae; Homo.
                                                                                                                                Q96FU5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022341; AAH22341.1; ... InterPro; IPR001278; Arg_tRNA-synt_1c. InterPro; IPR001412; tRNA-synt_1. Pfam; PF00750; tRNA-synt_1d; 1.
     Hypothetical
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TISSUE-Bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00178; AA_TRNA_LIGASE_I; ical protein.
578 AA; 65487 MW; 68BE
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                                                                                                                                                                                                                                                                                                           AVPIAQK 7
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Pred. No. 1.9e
1; Mismatches
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Pred. No. 1.2e
1; Mismatches
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1.9e+02;
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Q8ZJC4;
01-MAR-2002
01-MAR-2002
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J. Bacteriol. 184:4601-4611(2002).
EMBL; AJ414141; CAC89052.1; -.
EMBL; AE014001; AAM87516.1; -.
InterPro; IPR004771; K_eff.
InterPro; IPR006153; Na_H_porter.
InterPro; IPR006036; TrkA_Kuptake.
InterPro; IPR006036; TrkA_Kuptake.
InterPro; IPR003148; TrkA_N.
Pfam; PF00999: Na_H_porter.
                                                                                                                                                                                                                                                                                                                                                                        Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague" Rature 413:523-527(2001).
                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-KIM5 / BIOVAR Mediaevalis;
MEDLINE-22137863; PubMed=12142430;
MEDLINE-22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz
Fetherston J.D., Lindler L.E., Brubaker R.R., Pla
Straley S.C., McDonough K.A., Nilles M.L., Matson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBa
EMBL; BC010420; AAH10420.1; -.
InterPro; IPR001278; Arg_tRNA-synt_1c.
Pfam; PF00750; tRNA-synt_1d; 1.
PFINTS; PR01038; TRNASYNTHARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CO-92 / Biovar Orientalis;
MEDLINE-21470413; PubMed-11586360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable potassium-efflux system protein (K+ efflux,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia pestis.
Bacteria; Proteobacteria;
Enterobacteriaceae; Yersi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K+/H+ antiporter). KEFB OR YPO0191 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO0456; args; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yersinia
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D.C.,
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                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                          CR1.
                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Ceratotoxin 1 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beuve M., Lemaire O.;

Sugar beet-infecting beet western yellows virus (BWYV).

represents a distinct Polerovirus species.";

submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF473561; AAM22680.1; ...

InterPro; IPR000982; Luteo_ORF2.

Pfam; PF02122; Luteo_ORF2; 1.

PRINTS; PR0913; LVIRUSORF2.
                                                                                        "Evolution of the ceratotoxin gene family in the medfly Ceratitis capitata and the Natal fruit fly Ceratitis rosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00932; 2a37; Complete proteome. SEQUENCE 602 AA; 66328 P
                                                                                                                                                                                                                                                                                               Ceratitis rosa (Natal fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel 22, Last sequence up
01-MAR-2003 (TrEMBLrel 23, Last annotation
RNA-dependent RNA polymerase P1 protein
                                          Submitted (JUN-2001) to the EMBL; AJ272450; CAB75957.1;
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                             Tephritoidea;
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01-OCT-2002
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NON_TER
                                                                                                                                  Rosetto M.;
                                                                                                                                                                                                       NCBI_TaxID=56958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-directed RNA polymerase. SEQUENCE 635 AA; 69341 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=12042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beet western yellows virus
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S; PR00335; KUPTAKET
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(TrEMBLrel. 22,
(TrEMBLrel. 23,
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                                                                                                                                                                                                                               Tephritidae;
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                                                                                                                                                                                                                               Ceratitis
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                                                             EMBL/GenBank/DDBJ databases
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Pred. No. 2.1e+02;
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No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative genomic analysis of coexisting archaeal genetic variants in an antarctic marine microbial assemblage."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF393304; AAR76997.1; -. InterPro; IPR005814; Aminotrans_3.
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                                                                                  "Comparative genomic analysis of coexisting archaeal genetic in an antarctic marine microbial assemblage."; submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF393307; AAK76999.1; -.
                                                                                                                                                                                                                                                                  marine archaeal group NCBI_TaxID=166585;
                                                                                                                                                                                                                                                                                         Archaea; Crenarchaeota; marine archaeal group 1
                                                                                                                                                                                                                                                                                                                                        Glutamate semialdehyde aminotransferase uncultured crenarchaeote 83A10.
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NON_TER 197 197
SEQUENCE 197 AA; 22017 MW;
                                       InterPro; IPR005814; Aminotrans_3
Pfam; PF00202; aminotran_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=15G10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uncultured crenarchaeote 15G10
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                     Aminotransferase;
                                                                                                                                                                                Beja O.;
                                                                                                                                                                                                   STRAIN-83A10;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beja O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=166582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marine archaeal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 AVPVAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 AVPIAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AVPIAQK
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity 85.
6; Conservative
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Pred. No. 1.1e+02;
""" matches 0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C81B7D0C0D4AB270
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Q9YEC2;
Q1-NOV-1999
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01-MAR-2002
                                                                                     MEDLINE-99310339; PubMed-10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haik
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A.
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh y
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q977V9 PRELIMINARY; PRT; 198 AA. 0977V9; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) 61utamate semialdehyde aminotransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative genomic analysis of coexisting archaeal genetic variants in an antarctic marine microbial assemblage."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF393306; AAK76998.1; -. InterPro; IPR005814; Aminotrans_3. Pfam; PF00202; aminotran_3; 2.
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Archaea; Crenarchaeota; environmental samples;
marine archaeal group 1.
                                 crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-31B02;
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NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota;
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
1 protein APE0653.
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Ankai A., K
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Beja O., Koonin E.V., Araving L., ...

Bensen D.C., Feldman R.A., Swanson R.V., DeLong L...,

"Comparative genomic analysis of coexisting archaeal gen

"In an Antarctic marine microbial assemblage.";

I submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases

EMBL, AF93466, AAK96083 1;

R EMBL, AF93466, AAK96083 1;

R InterPro; IPR005814; Aminotrans_3.

Pfam; PF00202; aminotran_3; 1.

Pfam; PF00202; aminotran_3; 1.

Pfam; PF00202; aminotran_3; 1.

Prinotransferase; Transferase.

""inotransferase; Transferase."
                                                                                  MEDLINE=2433700.

The FANTOM Consortium,
The FANTOM Consortium,
The RATIKEN Genome Exploration Research Group Phr
The RIKEN Genome Exploration Research Group Phr
"Analysis of the mouse transcriptome based on
"60,770 full-length cDNAs.";
f 60,770 full-length cDNAs.";
RATURE 420::563-573/2002).
REMBL; ARO53482; BRC35757,1;
REMBL; ARO5482; BRC35757,1;
REMBL; 
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Search completed: September 12, 2003, 11:15:38
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GLPK_MYCPN
YTFM_ECOLI
DXS_ANASP
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O8u453 pyrococcus
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O3121 cottontail
P97303 mus musculu
Q9byv9 homo sapien
O4975 mycobacteri
P23052 berne virus
Q65900 c genome po
O66479 h genome po
O66479 h genome po
P44150 haemophilus
Q9cy88 lactococcus
Q9713 sulfolobus
P41218 homo sapien
P48629 spinacia ol
P75064 mycoplasma
P39320 escherichia
O8yz80 anabaena sp
P52850 mus musculu
P10394 drosophila
P5731 gallus gall
P7736 lactobacill
P7736 lactobacill
P77316 lactobacill
P77314 escherichia
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45	44	43	42	41	40	39	38	37	36	35	34
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Q91cc2 anabaena sp	P32796 saccharomyc	Q9wwg9 pseudomonas	Q07071 rattus norv	Q14397 homo sapien	060164 schizosacch	Q41438 solanum tub	P16893 plasmodium	Q97nv4 streptococc			P57312 buchnera ap

ALIGNMENTS

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CYTOCHROME CAPAR-I/CASPASE 9 PARHWAY. ACTS BY OPPOSING THE INHIBITORY ACTIVITY OF INHIBITOR OF APOPTOSIS PROTEINS (IAP). -!- SUBGNIT: Homodiner. Interacts with BIRC2, BIRC3, BIRC4/XIAP and BIRC7 (By similarity). -!- SUBCSLLULAR LOCATION: MITOCHONDRIAL BUT RELEASED INTO THE CYTOSOL WHEN CELLS UNDERGO APOPTOSIS. -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION FOUND IN HEART, LIVER,	KOhtsuki S.; "Functional annotation of a full-length mouse cDNA collection."; "Acture 409:685-690(2001). "I FUNCTION. DEDOCTES AND ACTIVATING CASPAGES IN THE	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF., Suzuki H., Toyo-Oka K., Wang K.H., Weltz C., Whittaker C., Wallining L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H.,	Sakal N., Okido T., Furuno M., Aono H., Baladrelli N., Balak J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,	Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissl C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,	MEDLINE=21085660; PubMed=11217851; Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,	proteins.";	9712; kusch M., Silke J., Con on R.J., Vaux D.L.; mammalian protein that	Mus musculus (Mouse). Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1] SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE	S CHOOL OF

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Best Local
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Suzuki Y., Ob
Nakamura Y.,
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2011 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Smac protein, mitochondrial precursor (Second mitochondria-derived activator of caspase) (Direct IAP binding protein with low pI).
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Alnemri E.S.;
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Mammalia; Eutheria;
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  TISSUE=Cerebellum;
                                                 "Molecular determinants of the
                                                                                PubMed=10950947;
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                                                                                                                                                                                                                          MEDLINE=20383536; PubMed=10929711;
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           EQUENCE FROM
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sit peptide; Mitochondrion;
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Q9NR28; 11
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AK012760;
                                                                                                                        human cDNA
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a mitochondrial protein that promotes cytochrome activation by eliminating IAP inhibition.";
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Catarrhini;
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ibahara T., T
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Koewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
LG1 Schutz J., Marra M.A.;
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamu
Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa
Kawakami B., Nagai K., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
                                                                                                                     This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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Herrmann J., Wu J.C., Fesik S
"Structural basis' for binding
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SUBCELLULAR LOCATION:
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ame=2; Synonyms=Diablo-S;
IsoId=Q9NR28-2; Sequence=VSP_004397
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STRAIN-JCM 10545 / 7;

MEDLINE-21456156; PubMed-11572479;

KAWARABAYSSI Y. Hino Y. Horikawa H. Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui ;

Sekine M., Baba K., Otsuka R., Nakazawa H., Takamiya M., Kal

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kal

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Ogu

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;
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 between
the Euro
                                                                                                             "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
-i- FUNCTION: This protein promotes the GTP-dependent trains.
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FUSA OR ST0437
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GO:0008625;
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1G3F; 10-JAN-01.
1G73; 10-JAN-01.
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BC004417;
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peptide; Mitochondrion; Apoptosis; Alternative spl
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BAB14994.1;
AAG22077.1;
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AAH04417.1;
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Pred. No. 2.7
0; Mismatches
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           ght. It is produced through Bioinformatics and the EN
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M., Kato Y.,
            EMBL
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              a collaboration
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InterPro; IPR005225; Small_GTP
Pfam; PF00579; EFG_C; 1.
Pfam; PF03764; EFG_IV; 1.
Pfam; PF00309; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNFCT;
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15-JUL-1998 (Rel. 36, 1
15-JUL-1998 (Rel. 36, 1
Ceratotoxin D precurson
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INIT_MET
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                                                                                                ceratotoxins are clustered in the genome of t capitata.";
Insect Biochem. Mol. Biol. 27:1039-1046(1997)
-i- FUNCTION: FEMALE-SPECIFIC PEPTIDES WITH P
                                                                                                                                                               TISSUE=Female accessory gland;
MEDLINE=98231103; PubMed=9569644;
Rosetto M., de Filippis T., Manet
                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyo
Tephritoidea; Tephritidae; Ceratitis.
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TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                          "The genes encoding
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                              CELSIUS.
SUBUNIT: HOME
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Whi

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hic

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Sa

Delcher A., Utterback T., Weldman J., Khouri H., Gill J.,
                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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ARCA OR RV1001 OR MT1030 OR MTCI237.16.
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Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y15375; CAA75598.1; -.
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                      non-profit institutions as long and this statement is not remove.
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                        statement is not removed.
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71
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     agreement (See
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t D., Hickey E.,
M.D., Salzberg
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RESULT 6
SYW_PYRAB
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Best Local :
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                                                                                                                                                                                                                                                                                                Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecon Poch O., Prieur D., Querellou J., Ripp R., Thlerry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; "An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi."; Mol. Microbiol. 47:1495-1512(2003).

-i- CATALUTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
                                                             PIR; C75020; C75020.

HAMAP; ME_00140; -; 1.

InterPro; IPR002305; tRNA-synt_1b.

InterPro; IPR001412; tRNA-synt_1.

InterPro; IPR002306; Trp_tRNA-synt_1b.

Pfam; PF00579; tRNA-synt_1b; 1.
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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or send an email t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UY11;
Complete
            Aminoacyl-tRNA synthetase;
                         TIGREAMS; TIGRO0233; trpS; 1. PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                    PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                 EMBL; AJ248288; CAB50601.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=12622808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRPS OR PYRAB16970
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HAMAP; ME_00242; -; 1.
InterPro; IPR003876; Arg_deiminase.
Pfam; PF02274; Amidinotransf; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota;
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01466; ARGDEIMINASE. TIGRFAMS; TIGRO1078; arca; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrpRS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z94752; CAB08144.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AVPIAQK
                                                                                                                                                                         s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41, Created)
41, Last sequence update)
42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR PAB1111.
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85.7%;
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              Protein biosynthesis;
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Pred. No.
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            Ligase;
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SYW_PYRUD

ID SYW_P

AC Q8U45

AC Q8U45

DT 28-FE

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RESULT 8
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation (Tryptophan--trna ligase)
                                                                                                                                                                                                                                              SITE
SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYRIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
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HAMAP; MF_00140; -; 1.
InterPro; IPR002305; tRNA-synt_Ib.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_Ib.
Pfam; PF00579; tRNA-synt_lb; 1.
TIGREAMS; TIGR00233; trpS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

"The complete sequence of the Pyrococcus furiosus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                   Complete
                                                                                                                                                                                                                                                                                                            PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase;
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257
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"KMSKS" REGION.
: 3A7A628958200CCC CRC64;
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"KMSKS" REGION
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                  386
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                                                                                                                                                                                                        Length 385;
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RESULT 9
VE2_CRPVK
VE2_CRPVK
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMPLETE sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).

-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) - AMP +
diphosphate + L-tryptophanyl-tRNA(Trp).

-!- SUBCELULLAR LOCATION: Cytoplasmic.
-!- SIMILBARITY: Belongs to class-I aminoacyl-tRNA synthetase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Takamiya M., Ohfuku Y., Yamazaki M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Oguchi A., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                  21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002306; Trp_tRNA-synt_1b.
Pfam; PF00579; tRNA-synt_1b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP000007; BAA31046.1; ALT_INIT. HAMAP; MF_00140; -; 1. Interpro; IPR002305; tRNA-synt_1b.
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Papillomavirus.
NCBI_TaxID=31553;
                                             Cottontail rabbit (shope) papillomavirus (strain Kansas)
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                               Probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                            165 AIPIAKK 171
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5; Conserv
                                                                                                               regulatory protein
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                                                                                                                                                                                                                               STANDARD;
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. 01, Last sequ
. 36, Last anno
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41. Last sequence update)
41. Last sequence update)
41. Last annotation update)
synthetase (EC 6.1.1.2) (Tryptophan--trNA ligase)
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257
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71.4%;
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"KMSKS" REGION.
; 9E3C392F4028B2DD CRC64.
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                                                                                                                                                            update)
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                                                                                                                                  update)
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62;
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(See http://www.isb-sib.ch/announce/
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         MEDILINE-97042438; PubMed-8887638;

Oyake T., Itoh K., Motohashi H., Hayashi N., Hoshino H., Yamamoto M., Igarashi K.;

"Bach proteins belong to a novel family of BTB-basic lettranscription factors that interact with Mafk and regulateranscription through the NF-E2 site.";

Mol. Cell. Biol. 16:6083-6095(1996).

-i- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS AS REFACTIVATOR. BINDS TO MAF RECOGNITION ELEMENTS (MARE).

BENDERGY ROLES IN COORDINATING TRANSCRIPTION ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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P97303;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDILINE-85166175; PubMed-2984661;
Giri I., Danos O., Yaniv M.;
Giri I., Danos O., Yaniv M.;
"Genomic structure of the cottontail rabbit (Shope) papillomavirus.";
"Proc. Natl. Acad. Sci. U.S.A. 82:1580-1584(1985),
-1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCUNNUNUNGGT-3') PRESENT
IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as rouse by non-profit institutions as rouse modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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the Euro
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InterPro; IPR000427; E2_C.
InterPro; IPR0001866; E2_N.
Ifam; PF00511; E2_C; 1.
Pfam; PF00508; E2_N; 1.
ProDom; PD000672; E2_C; 1.
ProDom; PD000678; E2_N; 1.
Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SEQUENCE 390 AA; 44024 MW; 8D6B35045E1B4B08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE
                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Transcription regulator protein BACH2 (BTB
                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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HSSP;
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                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                          BACH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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Rodentia;
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Pred. No.
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                TRANSCRIPTION ACTIVATION AND
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(BTB and CNC
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BAC2_HUMAN
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Best Local :
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
          SEQUENCE FROM N.A. (ISOFORM 1).
Melo J.V., Vieira S.D., Deininger M.W.N.;
"BACH2 expression in leukaemic cells.";
                                                        Nakahata T., Igarashi K., Yokoyan "Cloning and expression of human BACHZ mapped to chromosome 6q15."
Oncogene 19:3739-3749(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                     Sasaki S., Ito E., Toki T., Maekawa T., Ki
Muto A., Nagai H., Kinoshita T., Yamamoto
                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=20404861; PubMed=10949928;
                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50097; BTB; 1.
PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC;
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MGD; MGI:894679; Bach2.
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                                                                                                                                                                  NCBI_TaxID=9606;
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InterPro; IPR004827;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION:
-!- TISSUE SPECIFICITY: E:
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to SIMILARITY: Contains 1
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n; PF00170; bZIP; 1.
RT; SM00338; BRLZ; 1.
RT; SM00225; BTB; 1.
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37
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                                                                                                                                                                                                                                                                                                                                                     AIPVAEK 201
(FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
527
550
716 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                           Igarashi K., Yokoyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1FOS.
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        103
168
542
571
78935 .
                                                                                                                                                                                Primates;
                                                                                                                                                                                          Chordata;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BTB_
                                                                                                                                                                                                                                                                                                                                                                                                               84.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TF_bZIP.
the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _POZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activator; Repressor; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the bZIP family BTB/POZ domain
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                    Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                               BASIC MOTIF.
LEUCINE-ZIPPER.
; 9132B3731AE24333 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BTB.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28;
                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                B cell-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Maf-related transcription
                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.
                                                                                                                                                                                                                                                                                          841
                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                    Kanezaki R., V
to M., Inazawa
                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                             1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNC subfamily
                                                                                                                                                                                                                                CNC
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 716;
                                                                                                      R., Umenai T.,
azawa J., Taketo
                                                                                transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MONOCYTES
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                                                                                                                                                                                                                             homolog
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RESULT 12
METH_MYCLE
ID METH_M
AC Q49775
DT 15-JUL
DT 16-OCT
DT 16-OCT
                                                                                                                       DЬ
                                                                                                                                             Q
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Best Local S
Matches 4
METH_MYCLE STANDARD; PRT; 12
049775; 09CC37; 09S378;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                             CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PFUULIV, ELEZ; 1.
SMART; SM00338; BRLZ; 1.
SMART; SM00225; BTB; 1.
SMOCTTRE: PS50097; BTB; 1
                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000210; BTB POZ InterPro; IPR004827; TF_bZIP Pfam; PF00651; BTB; 1. Pfam; PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF357835; AAK48898.1;
EMBL; AJ271878; CAC28130.1;
EMBL; AL121787; CAB87587.1;
HSSP; P05412; 1FOS.
TRANSFAC; T04795; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                    Nuclear
                                                                                                                                                                                                                                                                                                                                                Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tromans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE OF 1-612
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note-No experimental confirmation available;
TISSUE SPECIFICITY: B-cell specific.
SIMILARITY: Belongs to the bZIP family. CNC su
SIMILARITY: Contains 1 BTB/POZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factors (By similarity).
SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitted (APR-2000) to the EMBL/GenBank/DDBJ databases. FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS AS REPRESSOR OR ACTIVATOR. BINDS TO MAF RECOGNITION ELEMENTS (MARE). PLAY IMPORTANT ROLES IN COORDINATING TRANSCRIPTION ACTIVATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Heterodimer of BACH2 and Maf-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPRESSION BY MAFK (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                       196 AIPVAEK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9BYV9-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:14078; BACH2.
                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                      c protein;
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [soId=Q9BYV9-2;
                                                                                                                                                                                      Similarity
                                                                                                                                                AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                           PS00036; BZIP_BASIC; 1.
                                                                                                                                                                                                                           291
841 AA;
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                               regulation; Activator;
                                                                                                                                                                                                                                                                                                                                    Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM
                                                                                                                                                                                                                                                                                                                                                                          BZIP;
                                                                                                                                                                                                                             291
92536
                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                      84.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TF_bZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence=VSP_000582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                     LEUCINE-ZIPPER.
Missing (in isoform 2
/FTId=VSP_000582.
L -> F (IN REF. 1).
                                                                                                                                                                         Score 28; DB
Pred. No. 1.3e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                   splicing.
                                                                                                                                                                                                                                                                                             BASIC MOTIF
                                                                                                                                                                                                                                                                                                          POLY-GLU.
                                                                                                                                                                                                                             4E926AC325952A93
                                                      1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family. CNC subfamily.
                                                                                                                                                                                                                                                                                                                                               Repressor; DNA-binding;
                                                                                                                                                                                                   DB 1;
                                                      Ą
                                                                                                                                                                                     3e+02
                                                                                                                                                                                                 Length 841;
                                                                                                                                                                                                                             CRC64;
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                                                                                          Query Match
Best Local :
Matches
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METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Whoseler P.R., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Bevlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Ouail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- COFACTOR: COBALAMIN (BY SIMILARITY).
-1- PATHWAY: TERMINAL STEP IN THE DE NOVO E
-1- SIMILARITY: BELONGS TO THE VITAMIN-B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + L-homocysteine tetrahydrofolate + L-methionine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) (Methionine synthase, vitamin-B12 dependent isozyme) (MS). METH OR ML1307 OR MLCB2533.04 OR B2126_C1_157.
                                                                                                                                  Transferase; Methyltransferase; Methionine biosynthesis; Vitamin Cobalt; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL035310; CAA22918.1; ALT_INIT. EMBL; AL583921; CAC31688.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U00017; AAA17182.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith D.R., Robison |
Submitted (MAR-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                                                       eproma; ML1307;
                                                                                                                                                             erPro; IPRO06158; B12-binding.
erPro; IPRO06158; CoMet_synt_B12.
erPro; IPR003759; CoMet_synt_B12.
erPro; IPR004223; Met_synt_B12.
erPro; IPR004223; Met_synt_B12.
erPro; IPR003726; S_methyl_trans.
m; PP02310; B12-binding; 1.
m; PP02507; B12-binding_2; 1.
m; PP025574; S-methyl_trans; 1.
m; PF02574; S-methyl_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHASE FAMILY.
CAUTION: REF.1 SEQUENCE DIFFERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAMESHIFT IN POSITION 873
                                                                                                                                                                                                                                                                                                                                                     E87072; E87072.
                                                                                                                                                                                                                                                                                                                                     P13009; 1BMT
 1 AVPIAQK 7
                              Similarity 5; Conser
                                                                                        753 7
1206 AA;
                               Conservative
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                                                                                          WW;
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                                            Score
Pred.
                                                                                       COBALAMIN-BINDING (POTENTIA COBALT (POTENTIAL).
MW; 7786CE5307D7CA86 CRC64;
                               Mismatches
                                         28;
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                         DB 1; 1.9e+02; 1;
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOSYNTHESIS OF METHIORINE
2 DEPENDENT METHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales;
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                                                          Length 1206
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341 AIPFAQK 347

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RESULT
POLG_CX
ID PO
AC Q6
DT 01
DT 01
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Best Local
POLG_CX16G
Q65900;
01-NOV-1997
01-NOV-1997
                                       _CX16G
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VIRUS PEDIOMER PROTEIN MEDIATES THE BINDING OF
-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE from ..... STRAIN-Isolate P138/72; STRAIN-Isolate P138/72; MEDLINE-91020973; Pubmed-2219698; Snijder E.J., den Boon J.A., Spaan W.J.M., "Primary structure and post-translational; "Primary structure and post-translational;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no Coronaviridae; Torovirus.
NCBI_TaxID=11156;
                                                                                                                                                                                                                                                                                                                                                                       EMBL; X52506; CAA36748.1;
                                                                                                                                                                                                                                                                                                                                                                                         e by non-profit institutions as long as its content is in no way dified and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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| VPVAQK 283
                                                                                                                         Similarity
                                                                                             VPIAQK 7
(Rel.
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                     Envelope
                             STANDARD;
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35,
                                                                                                                                                               1581
1572
272
384
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494
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1297
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1431
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Created)
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sequence update)
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Pred.
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on update)
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(GLCNAC.
(GLCNAC.
(GLCNAC.
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                                                                                                                                                                                                                                                                                                                                   GLYCOPROTEIN
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                                                                                                                         5e+02
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                                                                                                                                   1.
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                                                                                                                0
                                                                                                                                Length 1581;
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                                                                                                                Indels
                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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InterPro; IPR000081; Picc_P2A.
InterPro; IPR0002527; Picc_P2B.
InterPro; IPR001576; Rhv.
InterPro; IPR001676; RNA_Belicase.
InterPro; IPR007095; RNA_Del_DS_PS.
InterPro; IPR007095; RNA_Del_P3D.
InterPro; IPR0071205; RNA_Del_P3D.
InterPro; IPR007094; RNA_Del_P3D.
InterPro; IPR007094; RNA_Del_P3D.
InterPro; IPR0071205; RNA_Del_P3D.
InterPro; IPR0071205; RNA_Del_P3D.
InterPro; IPR0071205; RNA_Del_P3D.
InterPro; IPR00548; Cys-protease-3C; 1.
Pfam; PF001552; Picc_P2B; 1.
Pfam; PF001552; Picc_P2B; 1.
Pfam; PF001552; Picc_P2B; 1.
  RNA-directed
CHAIN
CHAIN
CHAIN 3
CHAIN 5
CHAIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; PF00947; Pico_P2A; 1.
pfam; PF01552; Pico_P2B; 1.
pfam; PF00073; rhv; 3.
pfam; PF00080; RNA_dep_RNA_pol;
pfam; PF00910; RNA_helicase; 1.
                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-2003 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Coat protein VP4 (PlA); Coat protein (PB); Coat protein VP5 (PlC); Coat protein VP1 (PlD); Core protein P2A; Core protein P2B; Core protein P2C; Core protein P3A; Genome-P2A; Core protein VP5 (P3B); Picornain 3C (EC 3.4.22.28) (Protease 3C) (P3C); RNA_directed RNA polymerase (EC 2.7.7.48) (P3D)].

(Coxsackievirus Al6 (strain G-10)
                                                                                                                       pfam; PF00910; RNA_helicase; 1.
Probom; PD001125; Cys_protease_3C;
Probom; PD001306; Ptoc_PzA; 1.
Probom; PD001274; Ptoc_P2B; 1.
                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; C03.022;
MEROPS; C03.UPA;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U05876; AAA50478.1; HSSP; P03300; 1POV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94303216; PubMed-8030260; Poyry T., Hyypiae T., Horsnell C., Kin Molecular analysis of coxsackievirus
                                                                                                Polyprotein;
                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=69159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: THE VIRUS CAPSID I EACH OF WHICH IS COMPOSED O VP3, AND VP4.
PTM: SPECIFIC ENZYMATIC CLE - SIMILARITY: THE PROTEASE BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             poliovirus polyprotein. In other picornavirus reactions Glu
substituted for Gln, and Ser or Thr for Gly.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [RNA](N).
                                                                                                            SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                    IPR003593; AAA_ATPase.
IPR000199; Cys_proteas
IPR003138; Pico_P1A.
     70
324
566
863
1013
                                                                                    RNA
                                                                                  polymerase;
                                                                                             protein;
    69
323
565
862
1012
1111
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                                                                                                                                                                                                                                                                                                                                                    Cys_protease_3C.
Pico_P1A.
ase; Hydrolase; Thiol pro
coat protein vp4.
COAT PROTEIN VP2.
COAT PROTEIN VP3.
COAT PROTEIN VP3.
COAT PROTEIN VP1.
CORE PROTEIN VP1.
CORE PROTEIN VP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLEAVAGES
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rus Al6 re
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                                                                                             Transferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EACH O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L., Hovi T.,
                                                                                 protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF PROTEINS VP1, VP2
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genetic g
                                                                                    Myristate
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Genome-
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2013 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Coat protein VP4 (P1A); Coat protein VP2 (P1B); Coat protein VP3 (P1C); Coat protein VP1 (P1D); Core protein P2A; Core protein P2B; Core protein P2C; Core protein P3A; Genome-11nked protein P2G (P3B); Ploornain 3C (EC 3.4.22.28) (Protease 3C)
11nked protein VP3 (Strain 7423/MS/87) (EC 2.7.7.48)].

Human enterovirus 71 (Strain 7423/MS/87) (EC 2.7.7.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLG_HE71M
Q66479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPID
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HE71M
                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VITUS RES. 39:195-206(1995).

-i- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
-i- CATALYTIC ACTIVITY: Selective cleavage of Gln-1-Gly bond in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown B.A., Pallansch M.A.; "Complete nucleotide sequence of enterovirus 71 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-96434998; PubMed-8837884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                               EMBL; U22522;
HSSP; P03300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              poliovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=103922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO IIELE FAMILY C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              poliovirus polyprotein. In other picornavirus reactions Glu may
substituted for Gln, and Ser or Thr for Gly.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: THE VIRUS CAPSID EACH OF WHICH IS COMPOSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1105 IPIAQK 1110
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5; Conserv
                                                                  p; IPR003593; AAA_ATPASE.
p; IPR00199; Cys_protease_3C.
p; IPR003138; Pico_P1A.
p; IPR000081; Pico_P2A.
p; IPR002527; Pico_P2B.
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1709
2193
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1441
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Rhv.
RNA_helicase.
RNA_pol_DS_PS.
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83.3%;
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PICORNAIN 3C.
RNA-DIRECTED RNA POLYMERASE.
MYRISTATE (BY SIMILARITY).
PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB Pred. No. 3.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS COMPOSED OF 60 ICOSAHEDRAL UNITS, OF ONE COPY EACH OF PROTEINS VP1, VF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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PROTEIN P3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
3.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stage; Picornaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATURE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VP1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Best Local S
Matches
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Pfam; PF00226; Pico_PIA; 1
Pfam; PF001572; Pico_P2B; 1
Pfam; PF001573; Pico_P2B; 1
Pfam; PF000773; rhy; 3.
                                                                    ACT_SITE
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ProDom; PD001306; Pico_P2A; 1.
ProDom; PD001274; Pico_P2B; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                           Pfam; PF00680; RNA_dep_RNA_pol; Pfam; PF00910; RNA_helicase; 1.
                                                                                                                                                                                                       RNA-directed RNA polymerase;
                                                                                                                                                                                                                 Polyprotein
                                                                                               LIPID
                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                   InterPro;
1105 IPIAQK 1110
                2 VPIAQK 7
                                   Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                IPR001205; RNA_pol_P3D.
IPR007094; RNA_pol_PSvir.
0548; Cys-protease-3C; 1.
                                                                             1695
1709
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566
863
1013
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1527
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1732
                                  Conservative
                                                                                                                                                                                                                 Coat
                                                                     ŘΑ;
                                                                             1695
1709
                                                                                                                 69
323
565
862
1012
1111
1440
1526
1548
1731
                                                                                                                                                                                                                 protein; Core protein; Transferase;
                                            84.8%;
                                                                     242656
                                                                                                                                COAT PROTEIN VP3.
COAT PROTEIN VP1.
CORE PROTEIN P2B.
CORE PROTEIN P2C.
CORE PROTEIN P2C.
CORE PROTEIN P3A.
                                                                     ¥.
                                           Score
Pred.
                                                                             MYRISTATE (BY SIMILARITY).
PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
                                                                                                       PICORNAIN 3C.
RNA-DIRECTED RNA POLYMERASE P3D.
                                                                                                                      GENOME-LINKED PROTEIN VPG.
                                                                                                                                                                                                         Hydrolase;
                                                                                                                                                                                                                                                                    1.
                                    Mismatches
                                                                     35E1B3CFF88A50EF CRC64;
                                                                                                                                                                                      PROTEIN VP4.
PROTEIN VP2.
                                           No.
                                                     DB 1;
                                            5e+02;
                                                                                                                                                                                                      protease; Myristate.
                                    0
                                                    Length 2193;
                                    Indels
                                    0
                                   Gaps
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Search completed: September 12, 2003, 11:13:55
Job time: 25 secs

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OM protein - protein search, using sw model
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
   Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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  length: 0
length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                       US-09-479-309-2
US-09-627-393-2
US-09-107-532A-7146
US-09-107-532A-7146
US-09-328-352-8139
US-08-752-307B-11
US-09-707-802-11
US-09-707-802-11
US-09-009-953-64
US-09-009-953-75
US-09-009-953-74
US-09-009-953-74
US-09-009-953-75
US-09-009-953-75
US-09-009-953-75
US-09-009-953-74
US-09-009-953-75
US-09-009-953-75
US-09-107-532A-413
US-09-117-784A-414
US-09-117-784A-413
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US-09-117-784A-5
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US-09-117-784A-5
US-09-38-352-7407
US-09-38-352-7407
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Sequence 2, Appli
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Sequence 25963, A
Sequence 2166, Ap
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 28, Appli
Sequence 28, Appli
Sequence 64, Appl
Sequence 64, Appl
Sequence 47, Appl
Sequence 474, Appl
Sequence 413, Appl
Sequence 413, Appl
Sequence 413, Appl
Sequence 14, Appli
Sequence 15, Appli
Sequence 16356, Ap
Sequence 1, Appli
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Query Match

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Score 33;

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Length 239;

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US-09-252-991A-25963
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GENERAL INFORMATION:
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107195.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25963
LENGTH: 629
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Best Local :
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Patent No. 6551795
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY_AGENT INFORMATION:
TELECOMMUNICATION
                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 AVPIAQ 205
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         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                     FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                          SOFTWARE: ASCII
                                                                                                                                                                                                                                         OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                               COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                           MEDIUM TYPE: CD/ROM ISO9660
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US-08-752-307B-11
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US-09-328-352-8139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQ ID NO 8139
; LENGTH: 326
; TYPE: PRT
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                                                                                                                                                                                                                                        Sequence 11, Application US/08752307B Patent No. 5952171
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATENT NO. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Acinetobacter baumannii
                                                                                                                                           APPLICANT: McCarthy, Sean A.
APPLICANT: Gearing, David P.
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7146:
SEQUENCE CHARACTERISTICS:
                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C
                                                                                                                                  NUMBER OF SEQUENCES:
COUNTRY: US
ZIP: 02110-2804
                                            STATE:
                                                           ADDRESSEE: Fish a ....
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                     294 IPVAQK 299
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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(B) LOCATION 1...1190
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85.7%;
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Pred. No. 1.4e+02;
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Pred. No. 3.6e+02;
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

OPERATING SYSTEM:

IBM Compatible

FastSEQ for Windows Version 2.0

US/08/752,307B

Windows95

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RESULT 7
US-09-707-802-11
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Best Local Similarity bo.,
The hes 4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08
FILING DATE: 19-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                        COMPUTER: IBM Compatible
operating SYSTEM: Windows 95
SOFTWARE: PSAtSEQ for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/707,802
FILING DATE: 07-No. 6391586-2000
CLASSIFICATION: <Unknown>
                                                 APPLICATION NUMBER: 08/752,307
FILING DATE: <Unknown>
ATTORNEY_AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
                                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ric
STREET: 225 Franklin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES ENCODING NOVEL SECRETED OR M
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
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lin Street
                                                                                                                                                                                                                                             for Windows Version
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Pred. No.
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2.9e+02;
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ
US-09-991-326-11
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US-09-991-326-11
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                                                                   Matches
                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 09404/020002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: FRSEISEQ for WINDOWS Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,326
FILING DATE: 21-No. 6395872-2001
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/752,307
FILING DATE: 19-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: McCarthy, Sean A. Gearing, David P.
488 IPVAQK 493
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STATE: MA
                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                            NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
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                                                                                                                                                                                                                     LENGTH: 612 amino acids
                                                                                                                                                                                                                                                                                       TELEFAX: 617-542-8906
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Pred. No. 2.
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Pred. No. 2.9e+02;
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US-09-009-953-8; Sequence 8, Application US/09009953; Patent No. 6413517; GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local (
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Cunningham, Bruce A.
APPLICANT: Crossin, Kathryn L.
TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE
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CITY: La Jolla
STATE: California
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fitting, Thomas REGISTRATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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   CURRENT
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 IPVAQK 493
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6313265
                                                                                                                                                                                                                                CITY: San Francisco
STATE: CA
SOFTWARE: FastSEQ fo
NT APPLICATION DATA:
                                                      OPERATING SYSTEM: DOS
                                                                                  COMPUTER: IBM Compatible
                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1268 amino acids
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NO: 28:
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                        for Windows Version 2.0
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Pred. No.
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,.6e+02;
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III REPEATS AND METHODS OF USE
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Patent No. 6413517
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Best Local
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APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 018623-011520US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ
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5; Conserv
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                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/036,713 FILING DATE: 23-JAN-1997 APPLICATION NUMBER: US 60/037,432 FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: CA
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                                                                                                          REFERENCE/DOCKET NUMBER: 018623-011520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                        TELEFAX: 415-576-0300
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71.4%;
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Identification of Broadly
Reactive DR Restricted Epitopes

Score 26; Pred. No.

DB 4;

Length 15; Indels

Mismatches

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Gaps

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ID NO:

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AVPLAMK 13

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; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-009-953-64
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US-09-009-953-64
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Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
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                                                   Matches
                                                                                    Query Match
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                                                                                                                                                                                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 64:
                                                  Local Similarity hes 5; Conserv
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                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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1 AVPIAQK 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CA
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/009,953 FILING DATE: 21-Jan-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVPLAMK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/036,713 FILING DATE: 23-JAN-1997
                                                                                                                                                                                                                        LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                            TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/037,432 FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                  Conservative
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71.4%;
                                                                78.8%;
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                                                              Score 26; DB 4; Length 15; Pred. No. 7.9;
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Pred. No. 7
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                                                  Mismatches
                                                                                                                                      64:
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7.9;
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RESULT 14
US-09-311-784A-414
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                                                                                                                                                   GENERAL INFORMATION:
                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                    Sequence 414, Application US/09311784A Patent No. 6534482
                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
                                                               APPLICANT:
                                          APPLICANT:
                                                                                                                                  APPLICANT: Fikes, John D.
                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 75:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
T: Chesnut, Robert W.
T: Epinmoune Inc.
INVENTION: Expression Vectors for Stimulating
                                                                                                                                                                                                                                                                                                                1 AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                           Ishioka, Glenn Y.
Livingston, Brian
                                                                                             Sette, Alessandro
                                                                                                               Hermanson, Gary G
                                                                                                                                                                                                                                                                                                                                                   Conservative
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                   Mismatches
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US-09-009-953-274
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                                                                                                                 PRIOR APPLICATION NUMBER: US 60/036,713

APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/037,432

FILING DATE: 07-FEB-1997

APTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REFERENCE/DOCKET NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-011520US

TELECOMMUNICATION INFORMATION:

TELEPAX: 415-576-0200

TELEFAX: 415-576-0300

TELEX: CUNKNOWN>

INFORMATION FOR SEO ID NO: 274:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids
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Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 414
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CURRENT APPLICATION NUMBER: US/99/311,784A
CURRENT FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/085,751 PRIOR FILING DATE: 1998-05-15
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 71.4%; hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                  MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 274:
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                                                            STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
                                                                                                          TYPE: amino acid
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Pred. No.
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Search completed: September 12, 2003, 11:16:12 Job time : 30 secs

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Result
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Maximum Match 10
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DB
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/Cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/Cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/Cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/Cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
/Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
/Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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   US-09-939-293-6

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US-10-293-371-24

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US-10-965-967-12

US-09-965-967-25

US-09-965-967-25

US-09-965-967-25

US-09-939-293-7

US-09-939-293-11

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Sequence 24, Appl
Sequence 45, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 25, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 9, Appli
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US-10-097-340-229	US-10-301-822-145	US-09-919-770-2	US-10-177-293-340	US-10-205-823-307	US-10-171-311-176	US-10-097-340-231	US-10-301-822-147	US-09-894-018-141	US-10-105-929-14	US-10-365-227-15	US-09-978-418-16	US-09-738-626-4863	US-10-079-167-95	US-09-894-018-274	US-10-156-761-7902	US-09-734-569-166	US-09-738-626-4488	US-09-734-569-94	us-10-156-761-7964	US-10-163-214-13	US-10-156-761-10999	US-09-252-088-39	US-09-252-088-44	US-10-153-668-348	US-10-141-618-14	us-09-798-116-4	US-09-798-116-2	US-09-925-297-591	US-09-798-116-7
Sequence 229, App	Sequence 145, App	Sequence 2, Appli	Sequence 340, App	307,	176,	Sequence 231, App	147,	Sequence 141, App	14,		16,	Sequence 4863, Ap	Sequence 95, Appl	Sequence 274, App	Sequence 7902, Ap	Sequence 166, App	Sequence 4488, Ap	Sequence 94, Appl	Sequence 7964, Ap					348,	14,	-	Sequence 2, Appli	Sequence 591, App	Sequence 7, Appli

ALIGNMENTS

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RESULT 2
US-09-965-967-8
; Sequence 8, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATENT NO. CALLED FOR PATENTION:
APPLICANT: ALIGENIA: Emad S.
TITLE OF INVENTION: AND METHODS OF USING THE SAME
TITLE OF INVENTION: AND METHODS OF USING THE SAME
FILE REFERENCE: 480140.465
CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DATE: 2001-08-24
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-939-293-6
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US-09-939-293-6
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LENGTH: 7
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1 AVPIAQK 7
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Pred. No. 4.8e+05;
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Sequence 24, Application US/10293371

Publication No. US20030157522A1

GENERAL INFORMATION:
APPLICANT: BOUDREAULT, ALAIN
APPLICANT: KORNELUK, ROBERT G.
APPLICANT: LACASSE, ERIC
APPLICANT: LISTON, PETER
TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
TITLE OF INVENTION: Interaction Screens
FILE REFERENCE: 07891/030002

CURRENT APPLICATION NUMBER: US/10/293,371

CURRENT APPLICATION SATE: 2003-04-08
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Best Local Similarity
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                                                                                                                                                                                                                                                  US-10-293-371-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic US-10-293-371-1
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Best Local S
Matches 7
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/293,371
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,934
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/332,300
PRIOR APPLICATION NUMBER: US 60/332,300
PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOUDREAULT, ALAIN
APPLICANT: KORNELUK, ROBERT G.
APPLICANT: LACASSE, ERIC
APPLICANT: LISTON, PETER
TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
TITLE OF INVENTION: Interaction Screens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/256,830
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
PRIOR APPLICATION NUMBER: US 60/370,934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No. 4.8e+05;
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Pred. No. 4.8e+05;
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Best Local Similarity
Thas 7; Conserve
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; OTHER INFORMATION: Synthetic
US-10-293-371-24
                                                                                                                                                                                                                         US-10-068-569-12
                                                                                                                                              Sequence 12, Application US/10068569
Publication No. US20020160975A1
GENERAL INFORMATION:
APPLICANT: Srinivasula, Srinivasa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
FILE REFERENCE: 480140.475
CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 28
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BOUDREAULT, ALAIN
APPLICANT: KORNELUK, ROBERT G.
APPLICANT: LACASSE, ERIC
APPLICANT: LISTON, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/370,934
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/332,300
PRIOR FILING DATE: 2001_11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/293,371
CURRENT FILING DATE: 2003-04-08
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PRIOR APPLICATION NUMBER: US 60/332,300
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 7
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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TYPE: PRT
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Pred. No.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-12
                                                                           ; ORGANISM: Drosophila melanogaster US-09-965-967-25
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-965-967-25
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                                                                                                             SEQ ID NO 25
LENGTH: 13
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/965,967
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,574
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/256,830
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09965967 Patent No. US20020177557A1
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Best Local Similarity 100.0%;
Matches 7; Conservative 0
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Patent No. US20020177557A1
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                                     Query Match
                                                                                                                                                                              APPLICANT: Shi, Yigong
TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis FILE REFERENCE: PU-0031 (01-1739-1)
CURRENT APPLICATION NUMBER: US/09/965,967
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,574
PRIOR APPLICATION NUMBER: 60/236,574
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 30
RUMBER OF SEQ ID NOS: 30
                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
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   Local Similarity nes 7; Conserv
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100.0%; Score 33; DB 1 ilarity 100.0%; Pred. No. 0.57; Conservative 0; Mismatches
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Pred. No. 0.44;
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Pred. No. 4.8e+05;
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                                    DB 10; Length 13;
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RESULT 11
US-09-939-293-7
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                                                                      GENERAL INFORMATION: APPLICANT: Alnemri,
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 15
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SEQ ID NO 8
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                          Sequence 7, Application US/09939293 Patent No. US20020132786A1
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TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
TITLE OF INVENTION: IAP-CASPASE INTERACTION
FILE REFERENCE: 480140.479
CURRENT APPLICATION NUMBER: US/10/197,634
CURRENT FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS FILE REFERENCE: 480140.475
CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 28
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TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE TITLE OF INVENTION: AND METHODS OF USING THE SAME FILE REFERENCE: 480140.465
CURRENT APPLICATION NUMBER: US/09/939,293
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Pred. No.
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Pred. No. 0.66;
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; LENGTH: 39
; TYPE: PRT
; ORGANIEM: Homo sapiens
US-09-939-293-8
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US-09-939-293-8
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TYPE: PRT;
ORGANISM: Homo sapiens
US-09-939-293-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-293-7,
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APPLICANT: Alnemri, Emad S.

APPLICANT: Alnemri, AN IAP PEPTIDE OR POLYPEPTIDE

TITLE OF INVENTION: AN LAT METHODS OF USING THE SAME

TITLE OF INVENTION: AND METHODS OF USING THE SAME

FILE REFERENCE: 480140.465

CURRENT APPLICATION NUMBER: US/09/939,293

CURRENT ETLING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                       Query Match
Best Local
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LENGTH: 35
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TITLE OF INVENTION: AN IAP PEPTIDE OR POLYDEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAMI
FILE REFERENCE: 480140.465
CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DATE: 2001-08-24
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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Pred. No. 1.8;
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Search completed: September 12, 2003, 11:17:31 Job time: 27 secs
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-293-2
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US-09-798-116-9
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US-09-939-293-2
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SEQ ID NO 9
LENGTH: 84
TYPE: PRT
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APPLICANT: Alhemi', Emad S.
TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAME
FILE REFERENCE: 480140.465
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Best Local
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APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
TITLE OF INVENTION: NO. US20020110851A1e1
FILE REFERENCE: 10338-004US
CURRENT APPLICATION UNMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 18
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Pred. No. 1.8;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 ,
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13.387 Million cell updates/sec
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33
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Human Smac protein
Human smac (DIABLO
                                                                                                               Human smac (DIABLO Human smac (DIABLO Human smac (DIABLO GIABLO G
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Human protein seques than protein seques than polypeptide Novel human enzyme Human smac (DIABLO Group B Streptococus polygroup	יוֹייִ עַ מַּ

ABB76213 standard; Peptide; 7

ALIGNMENTS

XX PA XX	XX XX	v PF	YY D	PN	H. L.	n 17	FH	XX	SO	XX	KW	XX	DE ^^	DT.	××	AC.	XX	RESU ABBI
(ABBO) ABBOTT LAB. Fesik SW, Meadows RP, Betz SP, Liu Z, Olejniczak ET, Sun	13-OCT-2000; 2000US-0687549.	12-OCT-2001; 2001WO-US32121.	18-APR-2002.	· WO200230959-A2.	e.g. C-terminal amide"	"ontional Caterminal	Key Location/Qualifiers	•	Homo sapiens.	numan; cancer; cycostatic; mutant; mutein.	DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;		Human smac (DIABLO) derived peptide.	09-AUG-2002 (first entry)		ABB76213;	•	RESULT 1 ABB76213 ID ABB76213 standard; Peptide; 7 AA.

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RESULT 2
AAUT8434
ID AAUT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of XIAP, an inhibitor of apoptosis protein (IAP) family member. Rd values for Bir-3 and Bir-2 are 0.70 +/- 0.09 uM and 9.4 +/- 0.6 uM, respectively, for the present (C-terminally amidated) peptide, compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac. Modification of the N-terminal alanine destroys binding affinity to XIAP, and mutation of the valine, proline or isoleucine also causes some loss of binding, Amino acids C-terminal to the isoleucine are not important for binding. The claimed peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac (DIABLO) peptide and an IAP
overexpresses inhibitor of caspase, modulating compounds
         Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                    WPI; 2002-304115/34.
                                                                                                                                                                                                                                                                          (UYJE-)
                                                                                                                                                                                                                                                                                                                                   24-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neoplastic cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2;
BC12 interacting domain; caspase; BIR domain; BIR3; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibitor of apoptosis (IAP) protein Smac,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU78434 standard; Peptide; 7 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                       JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                2000US-227735P.
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Pred. No.
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modulating compounds

23-AUG-2001; 2001WO-US41869

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RESULT 3
AAU78487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc cytoscilc Smac (a Smac isoform that begins with MKSDYFY sequence, creplacing the mitochondrial targeting sequence (residues 1-55 of (I)), cc and residues 5-60 of (I)) and an inhibitor of BID (BC12 interacting cdomain) with a compound to be tested for apoptotic inhibiting activity; (C) includating the cell populations with a direct stimulus of the cell death pathway; and (c) measuring the specific apoptotic activity is cell populations, where inhibition of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and polynuclectide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase, where the cell polynuclectide are cativity of caspase, where the cell inhibitor inhibits activation or activity of caspase. (I) and (II) is useful for identifying an inhibitor or enhancer of a caspase. (C) I is useful for identifying an inhibitor or enhancer of a caspase in cell viability indicates the presence of an inhibitor or candidate enhancer; and detecting cell viability, where an increase in cell viability indicates the presence of an enhancer. Optionally, the method involves detecting the presence of an enhancer of expressing (I), with the candidate compound. A decrease in processing indicates the presence of an enhancer of caspase of caspase. (I) are an enhancer or caspase in the presence of an enhancer of an enhancer of caspase in contacting cell transformed with the vector expressing cell caspase. (I) is also useful for contacting a compound that inhibits smac binding to smac-binding to smac-binding contacting of IRP. (II) is useful in gene therapy techniques. The contacting cell caspase in second of smac mutant the contacting cell caspase. (II) is useful in gene therapy techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                      Apoptosis; cytostatic; apoptotic; AV peptoid; melanoma; lymphoma; Inhibitor of Apoptosis protein; IAP; procaspase-3; tumour cell; breast cancer; prostate cancer; lung cancer; parcreatic cancer; smac-7; gastric cancer; colon cancer; ovarian cancer; renal cancer; hepatoma;
                                                                                                                                                                                                                                                                                                                Smac-7 AV peptoid.
                                                                                                     WO200216402-A2
                                                                                                                                               Synthetic
                                                                                                                                                                                         sarcoma;
                                                                                                                                                                                                                                                                                                                                                              18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                      AAU78487;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU78487 standard; Peptide; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated Smac peptide or polypeptide (I) and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising: (a) separately contacting several cell populations expressing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 7; 78pp; English
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                                                                                                                                                                                         smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVPIAQK 7
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                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                    cancer; ovarian cance
mitochondria-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 9.3e+05;
0; Mismatches 0;
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RRSULT 4
ABB761
ID ABB7
XX ABB76
AC ABB7
XX ABB7
XX ABB7
XX DIA
DE Huma
XX DIAE
KW huma
XX Homc
XX Hom
XX Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for enhancing the apoptosis of pathogenic cells, particularly tumour cells, e.g. breast cancer, prostate cancer, lung cancer, colon cancer, ovarian cancer or sarcoma, comprises apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogenic cells. The method comprises a novel pharmaceutical composition which comprises an AV peptoid in dosage form and a pharmaceutical carrier, where the AV peptoid comprises a peptide that interacts with or inhibits the activity of an Inhibitor of Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;
human; cancer; cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB76212 standard; Peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                13-OCT-2000; 2000US-0687549
                                                                                             12-OCT-2001; 2001WO-US32121
                                                                                                                                                                                                                       WO200230959-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human smac (DIABLO) derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Page 28; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2000; 2000US-0645075
                                                                                                                                                                                                                                                                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relates to a method for induction of apoptosis
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                           "optional C-terminal protecting e.g. C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 23; Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 5
ABB76209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            second mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI (DIABLO). The peptide is one of 12 claimed smac (DIABLO) derived peptides (see ABB/6208-19) which bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Kd values for Bir-3 and Bir2 are 0.80 +/- 0.3 uM and 13 +/- 0.3 uM, respectively, for the present (C-terminally amidated) peptide, compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac. Modification of the N-terminal alanine destroys binding affinity to XIAP, and mutation of the valine, proline or isoleucine also causes some loss of binding. Amino acids C-terminal to the isoleucine are not important for binding. The claimed peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel peptide derived from wild-type human second mitochondria activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                         12-OCT-2001; 2001WO-US32121
                                                                                                                                                                                                                                                                   DIABLO;
                                                                                                                                                                                                                                                                                              Human smac (DIABLO) derived peptide.
                                                                                                                                                                                                                                                                                                                           09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 7; 26pp; English.
           Fesik SW,
                                    (ABBO ) ABBOTT LAB
                                                               13-OCT-2000; 2000US-0687549
                                                                                                                     18-APR-2002.
                                                                                                                                               WO200230959-A2
                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                     ABB76209;
                                                                                                                                                                                                                                                                                                                                                                              ABB76209 standard; Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding interaction between a smac (DIABLO) peptide and an IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fesik SW,
                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tamily member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AVPIAQK 7
                                                                                                                                                                                                                                                                   smac; inhibitor of apoptosis protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVPIAQK
         Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                      cytostatic.
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                        /note= "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Betz SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide derived from wild-type human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
           SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu
         Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ζ,
         Ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 9.3e+05;
ches 0;
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         Olejniczak
                                                                                                                                                                                                                                                                   IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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         ET,
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           Sun
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Betz

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RESULT 6
ABB76229
ID ABB7
XX ABB7
AC ABB7
XX ABB7
XX DE Hum
XX DIA
KW DIA
KW DIA
KW hum
XX Hon
OS Sy1
XX Sy1
XX Sy1
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PT M1
FT M1
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FT M4
FT M4
FT M4
FT M5
FT M6
FT M7
XX AC
PN W
XX AC
PN M1
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XX AC
PN M3
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PN M4
XX AC
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XX AC
PN M7
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                           WPI; 2002-444169/47
                                                                                Fesik SW,
                                                                                                                                     (ABBO ) ABBOTT LAB
                                                                                                                                                                                          13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                                              12-OCT-2001;
                                                                                                                                                                                                                                                                                                   18-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB76229 standard; Peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIABLO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB76229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-444169/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 7; 26pp; English.
                                                                                Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                              2001WO-US32121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-terminal acetyl"
                                                                                Betz
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                                                                                SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                Liu
                                                                                Ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3e+05;
hes 0;
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                                                                                Olejniczak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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                                                                             ET,
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RESULT 7
ABB76228
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   direct inhibitor of apoptosis binding protein with low pi (DIABLO), but with the native N-terminal alanine residue (see ABB76209) acetylated. Claimed smac-derived peptides (see ABB76208-19) bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Modification of the N-terminal alanine destroys all binding affinity for the protein. Thus, Kd values for Bir-3 and Bir-2 were each over 1,000 uM for the present peptide, compared with 0.43 +/- 0.06 uM and 6.0 +/- 0.9 uM, respectively, for the corresponding wild-type peptide. The claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac peptide and an IAP
                     Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                              WPI; 2002-444169/47.
                                                                                                        Fesik
                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                   (ABBO ) ABBOTT LAB
                                                                                                                                                             13-OCT-2000; 2000US-0687549
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                                                                                                                                                                                                                                                WO200230959-A2
                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         human; cancer;
                                                                                                                                                                                                                                                                                                                                                                                       DIABLO; smac;
                                                                                                                                                                                                                                                                                                                                                                                                                Fluorosceinated smac (DIABLO) derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB76228 standard; Peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a peptide derived from human semitochondria derived activator of caspase (smac), also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 15; 26pp; English.
                                                                                                          SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             member.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                        Meadows
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   inhibitor of apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                         cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                                          /note= "N-terminal fluorescein"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Pred. No. 9.3
0; Mismatches
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                                                                                                        Olejniczak
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Example 1; Page 14; 26pp; English

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RESULT 8
ABP713144
ID ABP71314
ABP713144
ID ABP7
XX ABP7
XX ABP7
XX On 11
XX On 11
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XX VASS
YX HOM
XX VASS
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YX 15-,
YX 113-,
YX 113-
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Best Local
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The invention relates to polynucleotides encoding an Omi (serine protease) peptide or polypeptide. The Omi peptide specifically binds to portion of an Inhibitor of Apoptosis Protein (IRP). The Omi polypeptide induces caspase-independent apoptosis, or fails to have serine protease activity. The Omi peptides are useful for regulating or altering apoptosis, specifically caspase-mediated apoptosis, and as immunogens for raising antibodies. Enhancers of apoptosis are useful for treating cancers, tumours or for destroying cells that mediate autoimmune diseases. Compositions may also be used for the treatment of diseases associated with inappropriate activation of apoptosis such as neurodegenerative diseases and ischaemic injury. The antibodies can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence corresponds to amino acids 1-9 of human second mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI (DIABLO), but is fluorosceinated. The peptide was used in a fluorescence polarisation-based competition assay designed to determine the binding affinity of variant smac peptides (see ABB76206-27) to the Bir-3 and Bir-2 domains of XIAP, an inhibitor of apoptosis protein (IAP) family member. Claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                                                                                    New Omi nucleic acids and peptides that bind apoptosis proteins, useful for regulating or apoptosis and for treating cancer, tumor, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUL-2001;
14-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003006680-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2002; 2002WO-US22658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HtrA2; serine protease; inhibitor of apoptosis protein; IAP;
ase; apoptosis; cytostatic; immunosuppressive; neuroprotective;
tropic; gene therapy; Smac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-221760/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                              Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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2001US-340163P.
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                                                                                                                                                                                                                                                                                                                                                              6; 83pp; English
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 26;
                                                                                                                                                                                                                                                                                                                                                                                                                       altering caspase-mediated autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 9
ABB76208
ID ABB76208
ID ABB7
XX ABB7
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XX DIAB
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KW DIAB
KW DIAB
KW Huma
XX Homc

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The present sequence is a peptide derived from wild-type human second mitochondria derived activator of caspase (smac), also known as direct inhibitor of appotosis binding protein with low put (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived peptides (see ABB76208-19) which bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of appotosis protein (IAP) family member. Rd values for Bir-3 and Bir-2 are 0.69 +/- 0.05 uM and 6.7 +/- 0.7 uM, respectively, for the present peptide, compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac. Modification of the N-terminal alanine destroys binding affinity to XIAP. For example, N-terminal alanine destroys binding affinity to XIAP. For example, N-terminal acetylation of the present peptide, or isobityric acid all resulted in Kd values for Bir-3 and for Bir-2 of over 1.000 uM. The claimed peptides can be used to identify the assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac (DIABLO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide derived from wild-type human second activator of caspase protein useful for identifying substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 7; 26pp; English.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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RESULT 10
AAU78435
ID AAU78435
XX AAU78
XX Inhib
XX Human
KW Bcl2
XX Homo
OS Synth
YX WO20C
XX 10-10
PF 24-AI
XX XX 24-AI
XX XX 24-AI
XX X Inher
XX PF IOT:
PT MOULT
PT MOULT
XX WPI;
XX PT OVE:
PT OV
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CC and an isolated nucleic acid (II) encoding (I). Also described is a CC method of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (BC12 interacting activity; CC domain) with a compound to be tested for apoptotic inhibiting activity; CC (b) incubating the cell populations with a direct stimulus of the cell cell populations, where inhibition of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptosis. (I) and (II) CC are useful for inducing apoptosis in a cell. The Smac polypeptide and CC polynucleotide are useful for stimulating apoptosis in a neoplastic or compared inhibitor inhibits activation or activity of caspase-3, preferably, the cell overexpresses at least a portion of IAP. CC inhibitor inhibits activation or activity of caspase-3 caspase-7 or caspase-9, preferably, the cell overexpresses at least a portion of IAP. CC inhibitor inhibits activation or activity of caspase-3 caspase-7 or caspase-9 the activation or activity of caspase-3 caspase-7 or caspase-9 than a condidate inhibitor or enhancer of a caspase-1 and the activation or activity of caspase-3 caspas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
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neoplastic cell; mutant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-304115/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; 78pp; English
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Pred. No. 0.
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RESULT 11
AAU78439
ID AAU78439
XX AAU788
XX Inhib
XX Inhib
XX Human
KW Bcl1
XX Bcl2
XX NC200
XX Homo
PN WC200
XX 24-AU
XX 24-AU
XX PP 24-AU
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PT Novel
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PT Novel
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Best Local S
Matches 7
                    The invention relates to an isolated Smac peptide or polypeptide (I) and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising: (a) separately contacting several cell populations expressing a cytosolic Smac isoform that begins with MKSDFYF sequence, replacing the mitochondrial targetting sequence (residues 1-55 of (I)), and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting domain) with a compound to be tested for apoptotic inhibiting activity: (b) incubating the cell populations with a direct stimulus of the cell death pathway; and (c) measuring the specific apoptotic activity is cell populations, where inhibition of the specific apoptotic activity is reflective that the compound is an inhibitor of apoptotic activity is considered in the that the compound is an inhibitor of activity is and in the specific apoptotic activity is considered in the specific apoptotic activity is considered in the specific apoptotic activity is considered in the specific apoptotic activity is considered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method involves detecting the presence of large and small caspase subunits after contacting cell transformed with the vector expressing (I), with the candidate compound. A decrease in processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small subunits of caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for identifying a compound that inhibits Smac binding to Smac-binding molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR2 or BIR3, or a full-length IAP). (II) is useful in gene therapy techniques. The present sequence represents the amino acid sequence of Smac mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alnemri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2; Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy; neoplastic cell; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU78439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 47; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulating compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-304115/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smac-N30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US26492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
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Pred. No. 0.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23
0.91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
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of.

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RESULT 12
AAU78436
ID AAU78
XX AU78
AC AAU78
AC AAU78
AC Inhib
XX Inhib
XX Inhib
XX Human
KW Bcl2
KW neop1
XX Neop1
OS Synth
XX Neop2
KW Neop2
CX Synth
PF 24-AU
XX 24-AU
XX 24-AU
XX 24-AU
XX Alnem
XX WPI;
XX WPI;
XX WPI;
XX WPI;
YX Nove]
PT Nove]
PT Nove]
PT modul
XX Examp
XX Examp
XX The :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC are useful for inducing apoptosis in a cell. The Smac polypeptide and CC polynucleotide are useful for stimulating apoptosis in a neoplastic or CC tumour cell which overexpresses an inhibitor of caspase, where the CC inhibitor inhibits activation or activity of caspase-3, caspase-7 or CC (I) is useful for identifying an inhibitor or enhancer of a caspase-CC mediated apoptosis which involves contacting a cell transfermed or CC transfected with a vector expressing (I) with a candidate inhibitor or CC transfected with a vector expressing (I) with a candidate inhibitor or CC candidate enhancer; and detecting cell viability, where an increase in CC cell viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an enhancer. Optionally, the CC method involves detecting cell transformed with the vector expressing (I) with the candidate compound. A decrease in processing indicates the presence of an inhibitor and an increase in the processing indicates the CC presence of an enhancer. Preferably, the large and small subunits of CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for CC identifying a compound that inhibits smac binding to Smac-binding CC molecule (a portion of IAPe. 9; a BIR domain such as BIR? DIRZ or BIR3, or a full-length IAP). (II) is useful in gene therapy techniques. The CC present sequence represents the amino acid sequence of Smac peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                   Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2; Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy; neoplastic cell; mutant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200216418-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU78436 standard; Peptide; 39
The invention relates to an isolated Smac peptide or polypeptide (I)
                                           Example 3; Fig 7; 78pp; English.
                                                                                                                                                                                       WPI; 2002-304115/34
                                                                                                                                                                                                                                                                         (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                  24-AUG-2000; 2000US-227735P
                                                                                                                                                                                                                                                                                                                                                         24-AUG-2001; 2001WO-US26492
                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVPIAQK 7
                                                                                  compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 13
AAU78430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC replacing the mitochondrial targeting sequence (residues 1-55 of (1)), and an inhibitor of BID (BCL2 interacting cdomain) with a compound to be tested for apoptotic inhibiting activity; (CC (b) incubating the cell populations with a direct stimulus of the cell coell populations, where inhibition of the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity of the cell populations, where inhibition of the specific apoptosis (I) and (II) (CC are useful for inducing apoptosis in a cell. The Smac polypeptide and CC polypucleotide are useful for stimulating apoptosis in a neoplastic or CC tumour cell which overexpresses an inhibitor of caspase, where the CC inhibitor inhibits activation or activity of caspase, where the CC inhibitor inhibits activation or activity of caspase, where the CC inhibitor inhibits activation or activity of caspase, where the CC inhibitor inhibits which involves contacting a cell transformed or CC caspase Preferably, the cell overexpresses at least a portion of IAP. CC (I) is useful for identifying an inhibitor or enhancer of a caspase or CC candidate enhancer; and detecting cell viability, where an increase in CC cell viability indicates the presence of an inhibitor and a decrease in cell viability, indicates the presence of an enhancer. Optionally, the presence of an enhancer of an inhibitor and a increase in the processing indicates the CC presence of an enhancer. Preferably, the large and small subunits of CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for CC dentifying a compound that inhibits smac binding to Smac-binding CC molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR OF BIR3, or a full-length IAP). (II) is useful in gene therapy techniques. The CC Smac-N39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                       Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2;
Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising:
(a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence,
                                                          (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                  WO200216418-A2
                                                                                                                                                                                                                                                                                                                   neoplastic cell;
                                                                                                                                                                                                                                                                                                                                                                                                      Inhibitor of apoptosis (IAP) protein Smac, N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU78430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU78430 standard; Peptide; 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                  24-AUG-2000;
                                                                                                                                             24-AUG-2001; 2001WO-US26492
                                                                                                                                                                                        28-FEB-2002
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                  2000US-227735P
                                                                                                                                                                                                                                                                                                                   tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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RESULT 14
ABG72303
ID ABG72
XX ID Rat F
XX Rat;
KW Inhil
KW INHIL
KW AUCOL
KW AUCOL
KW AUCOL
XX ATTOL
XX RATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC death pathway; and (c) measuring the specific apoptotic activity of the C cell populations, where inhibition of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptotic activity is C indicative that the compound is an inhibitor of apoptotic activity is C are useful for inducing apoptosis in a cell. The Smac polypeptide and (II) CC are useful for inducing apoptosis in a cell. The Smac polypeptide and C polynucleotide are useful for stimulating apoptosis in a neoplastic or C tumour cell which overexpresses an inhibitor of caspase, where the C caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-7 or CC transfected with a vector expressing (I) with a candidate inhibitor or CC transfected with a vector expressing (I) with a candidate inhibitor or CC candidate enhancer; and detecting cell viability, where an increase in CC cell viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an enhancer. Optionally, the CC method involves detecting cell transformed with the vector expressing (C (I)) with the candidate compound. A decrease in processing indicates the presence of an inhibitor and a increase in the processing indicates the presence of an enhancer. Preferably, the large and small caspase the C presence of an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small subunits of C caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for C caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for C caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for Or caspase-7 or caspase-9 are detected. (I) is also useful for C caspase-1, caspase-7 or caspase-9 are detected. (I) is also useful for C dentifying a compound that inhibits smac binding to Smac-binding to Smac-binding to Smac-binding to Smac-binding to Smac-binding to Smac-binding to Smac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                             Rattus
                                                                                                      autoimmune disease; neurodegenerative
muscular tissue damage; heart attack;
                                                                                 liver disease;
                                                                                                                                                                                                                                        Rat partial
                                                                                                                                                                                                                                                                                            29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replacing the mitochondrial targeting sequence (residues 1-55 of (I)), and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting domain) with a compound to be tested for apoptotic inhibiting activity; (b) incubating the cell populations with a direct stimulus of the cell contains the cell population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising: (a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence,
                                                                                                                            Rat; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic disease; autoimmune disease; neurodegenerative disease; tissue damage;
                                                                                                                                                                                                                                                                                                                                             ABG72303
                                                                                                                                                                                                                                                                                                                                                                                                ABG72303 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 7; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overexpresses inhibitor of caspase, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents the N-terminal amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to an isolated Smac peptide or polypeptide (an isolated nucleic acid (II) encoding (I). Also described is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptides and polynucleotides encoding the peptides, useful
ating apoptosis in neoplastic or tumour cell which
ses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                   sequence for pro-apoptotic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                Protein; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                         hepatic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                      DIABLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s (I)
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RESULT 15
ABG72302
В
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                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated pro-apoptotic polypeptide, CC designated DIABLO, or its biologically active fragment of 8 amino acids in length. Also included are the polynucleotide encoding DIABLO, CC expression vectors, transformed host cells, producing a biologically contive fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP) with a fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP) continuing a natural or synthetic variant of DIABLO (continuing a cell with a natural or synthetic variant of DIABLO (continuing a cell with an interest proposed (continuing a cell with an interest proposed (contacting and activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO related (condition comprising an agent which reduces the level/activity of a polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is a condition associated with expression or activation of DIABLO, such as cancer, vascular consistency of a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with heart contact, or hepatic disease, autoimmune disease and neurodegenerative contacts of a polypeptide comprised or muscular tissue damage associated with heart contacts, or hepatic tissue damage associated with a liver disease.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence
                                                                                                            29-JAN-2003
                                                                                                                                                                                   ABG72302 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 35; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2001; 2001US-0798116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verhagen AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HALL-) HALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002110851-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                represents
                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-074681/07
                                                                   partial sequence for pro-apoptotic protein DIABLO
                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or apoptosis e.g. cancer
                                                                                                                                                                                                                                                                                                               1 AVPIAQK 7
                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conser
                                                                                                                                                                                                                                                                              AVPIAQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                              partial
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000AU-0005995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ekert PG,
                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaux DL;
                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                     Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         DB 24;
                                                                                                                                                                                                                                                                                                                                                                   .9;
                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                     Length 84;
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                                                                                                                                                                                                                                                                                                                                                    Gaps
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Human; pro-apoptotic protein; DIABLO; cell death; apoptosis;

inhibitor of apoptosis; IAP; cancer; vascular disease; hepati autoimmune disease; neurodegenerative disease; tissue damage;

hepatic

disease;

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Search completed: September 12, 2003, 11:13:24 Job time: 84 secs
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with an TAP and detecting the presence of an TAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO related condition comprising an agent which reduces the level/activity of a polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen-binding molecule is useful for detecting DIABLO in a biological sample. The agent which modulates the level and/or functional activity of a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular diseases and neurodemorative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino acids in length. Also included are the polynucleotide encoding DIABLO, expression vectors, transformed host cells, producing a biologically active fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP) with a fragment of the polypeptide, and detecting a reduction in activity of the IAP), producing a natural or synthetic variant of DIABLO with cell death activity or which reduces IAP activity, an antigenbinding molecule that specifically binds to DIABLO or its fragment, detecting DIABLO in a biological sample (by contacting the sample activity or which reduces the detecting the sample of the detecting the sample of the detecting the sample of the detection of the detection of the sample of the detection of the de
                                                                                                                                                                                                                                                                                                                                                                                             disease, hepatic disease, autoimmune disease and neurodegenerative disease, tissue damage or muscular tissue damage associated with heart attack, or hepatic tissue damage associated with a liver disease. DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence represents partial human DIABLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell death or apoptosis e.g. cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2E; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-074681/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2001; 2001US-0798116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2002110851-A1.
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                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verhagen AM, Ekert PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000; 2000AU-0005995.
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                                                                                                                                                                                                                            Local Similarity
nes 7; Conserv
                                                                                                                 19
                                                                                                                                                                      1 AVPIAQK 7
                                                                                                              AVPIAQK 25
                                                                                                                                                                                                                                                                                                                                                202 AA;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen
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26..202
/label- Mature_DIABLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaux DL;
                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                          Score 33;
Pred. No.
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                              DB 24; Length 202;
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                               0;
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